A1 Cont.

3. The method of claim 1, wherein at least one of the two or more heterologous nucleic acid sequences is modified after cojoining the two or more heterologous nucleic acid sequences.

4. The method of claim 1, wherein the one or more enzymatic domains participate in a same metabolic pathway.

5. The method of claim 1, wherein at least one of the two or more heterologous nucleic acid sequences is modified by shuffling at least one nucleic acid sequence.

A2

7. The method of claim 1, wherein the two or more heterologous nucleic acid sequences encode enzymatic domains selected from the group consisting of phytoene synthase, phytoene desaturase, z-carotene desaturase, and beta-cyclase.

8. The method of claim 1, wherein the two or more heterologous nucleic acid sequences encode enzymatic domains selected from the group consisting of diaminobutyric acid aminotransferase, diaminobutyric acid acetyltransferase, and ectoine synthase.

9. The method of claim 1, wherein the two or more heterologous nucleic acid sequences encode enzymatic domains selected from the group consisting of beta-ketothiolase, D-reductase, and poly(hydroxyalkanoate) synthase.

10. The method of claim 1, wherein the two or more heterologous nucleic acid sequences encode enzymatic domains selected from the group consisting of a ketosynthase-acyltransferase, a chain length factor, an acyl carrier protein, and a cyclase.

11. The method of claim 1, wherein cojoining the two or more heterologous nucleic acid sequences comprises connecting the two or more heterologous nucleic acid sequences directly to one another.

12. The method of claim 1, wherein cojoining the two or more heterologous nucleic acid sequences comprises connecting the two or more heterologous nucleic acid sequences with one or more nucleotide linker sequences.

A3

19. The method of claim 1, wherein the modified gene fusion construct further comprises one or more transcription regulatory sequences.

A4

23. The method of claim 22, wherein the plant system is selected from the group consisting of Fragaria, Lotus, Medicago, Onobrychis, Trifolium, Trigonella, Vigna, Citrus, Linum, Geranium, Manihot, Daucus, Arabidopsis, Brassica, Raphanus, Sinapis, Atropa,

A4 CON'T.

Capsicum, Hyoscyamus, Lycopersicon, Nicotiana, Solanum, Petunia, Digitalis, Majorana, Cichorium, Helianthus, Lactuca, Bromus, Asparagus, Antirrhinum, Hererocallis, Nemesia, Pelargonium, Panicum, Pennisetum, Ranunculus, Senecio, Salpiglossis, Cucumis, Browaalia, Glycine, Lolium, Zea, Triticum, Sorghum, Malus, Apium, Narcissus, Docus, and Datura.

25. A modified gene fusion construct comprising two or more cojoined heterologous nucleic acid sequences, wherein each nucleic acid sequence encodes one or more enzymatic domains, and wherein at least one of the two or more cojoined heterologous nucleic acid sequences is modified.

26. The modified gene construct of claim 25, wherein at least one of the two or more cojoined heterologous nucleic acid sequences is shuffled.

27. The modified gene fusion construct of claim 25, wherein the two or more cojoined heterologous nucleic acid sequences encode at least two enzymatic domains selected from the group consisting of phytoene synthase, phytoene desaturase, z-carotene desaturase, and beta-cyclase.

A5

28. The modified gene fusion construct of claim 25, wherein the two or more cojoined nucleic acid sequences encode at least two enzymatic domains selected from the group consisting of diaminobutyric acid aminotransferase, diaminobutyric acid acetyltransferase, and ectoine synthase.

29. The modified gene fusion construct of claim 25, wherein the two or more cojoined heterologous nucleic acid sequences encode at least two enzymatic domains selected from the group consisting of beta-ketothiolase, D-reductase, and poly(hydroxyalkanoate) synthase.

30. The modified gene fusion construct of claim 25, wherein the two or more cojoined heterologous nucleic acid sequences encode at least two enzymatic domains selected from the group consisting of a ketosynthase-acyltransferase, a chain length factor, an acyl carrier protein, and a cyclase.

A6

38. The method of claim 32, wherein at least one of the cojoined heterologous nucleic acid sequences is modified.

39. The method of claim 38, wherein at least one of the cojoined heterologous nucleic acid sequences is shuffled.

40. The method of claim 32, wherein the two or more heterologous nucleic acid sequences encode enzymatic domains selected from the group consisting of phytoene synthase, phytoene desaturase, z-carotene desaturase, and beta-cyclase.

41. The method of claim 32, wherein the two or more heterologous nucleic acid sequences encode enzymatic domains selected from the group consisting of diaminobutyric acid aminotransferase, diaminobutyric acid acetyltransferase, and ectoine synthase.

A6 CONT.

42. The method of claim 32, wherein the two or more heterologous nucleic acid sequences encode enzymatic domains selected from the group consisting of beta-ketothiolase, D-reductase, and poly(hydroxyalkanoate) synthase.

43. The method of claim 32, wherein the two or more heterologous nucleic acid sequences encode enzymatic domains selected from the group consisting of a ketosynthase-acyltransferase, a chain length factor, an acyl carrier protein, and a cyclase.

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46. The method of claim 32, wherein the modified gene fusion construct further comprises one or more transcription regulatory sequences.

A8

50. The method of claim 49, wherein the plant system is selected from the group consisting of Fragaria, Lotus, Medicago, Onobrychis, Trifolium, Trigonella, Vigna, Citrus, Linum, Geranium, Manihot, Daucus, Arabidopsis, Brassica, Raphanus, Sinapis, Atropa, Capsicum, Hyoscyamus, Lycopersicon, Nicotiana, Solanum, Petunia, Digitalis, Majorana, Cichorium, Helianthus, Lactuca, Bromus, Asparagus, Antirrhinum, Hererocallis, Nemesia, Pelargonium, Panicum, Pennisetum, Ranunculus, Senecio, Salpiglossis, Cucumis, Browaalia, Glycine, Lolium, Zea, Triticum, Sorghum, Malus, Apium, Narcissus, Docus, and Datura.

A9

52. A gene fusion construct comprising two or more cojoined heterologous nucleic acid sequences that participate in the same metabolic pathway, wherein at least one of the cojoined heterologous nucleic acid sequences is derived from a eukaryote and another cojoined heterologous nucleic acid sequence is derived from either a different species of eukaryote or from a prokaryote.

53. The gene fusion construct of claim 52, wherein at least one of the cojoined heterologous nucleic acid sequences is modified.

54. The gene fusion construct of claim 53, wherein at least one of the cojoined heterologous nucleic acid sequences is shuffled.

55. The gene fusion construct of claim 52, wherein the two or more cojoined heterologous nucleic acid sequences encode at least two enzymatic domains selected from the group consisting of phytoene synthase, phytoene desaturase, z-carotene desaturase, and beta-cyclase.

56. The gene fusion construct of claim 52, wherein the two or more cojoined heterologous nucleic acid sequences encode at least two enzymatic domains selected from the group consisting of diaminobutyric acid aminotransferase, diaminobutyric acid acetyltransferase, and ectoine synthase.

57. The gene fusion construct of claim 52, wherein the two or more cojoined heterologous nucleic acid sequences encode at least two enzymatic domains selected from the group consisting of beta-ketothiolase, D-reductase, and poly(hydroxyalkanoate) synthase.

A9 CON't.

58. The gene fusion construct of claim 52, wherein the two or more cojoined heterologous nucleic acid sequences encode at least two enzymatic domains selected from the group consisting of a ketosynthase-acyltransferase, a chain length factor, an acyl carrier protein, and a cyclase.

59. A vector comprising the gene fusion construct of claim 52 and a promoter.

60. A gene fusion construct comprising two or more cojoined heterologous nucleic acid sequences, wherein the two or more cojoined heterologous nucleic acid sequences encode at least two enzymatic domains selected from the group consisting of diaminobutyric acid aminotransferase, diaminobutyric acid acetyltransferase, and ectoine synthase.

61. The gene fusion construct of claim 60, wherein at least one of the two or more cojoined heterologous nucleic acid sequences is modified.

62. The gene fusion construct of claim 61, wherein at least one of the two or more cojoined heterologous nucleic acid sequences is shuffled.

63. A gene fusion construct comprising three or more cojoined heterologous nucleic acid sequences, wherein the three or more cojoined heterologous nucleic acid sequences encode at least three enzymatic domains selected from the group consisting of beta-ketothiolase, D-reductase, and poly(hydroxyalkanoate) synthase.

64. The gene fusion construct of claim 63, wherein at least one of the three or more cojoined heterologous nucleic acid sequences is modified.

65. The gene fusion construct of claim 64, wherein at least one of the three or more cojoined heterologous nucleic acid sequences is shuffled.

66. A gene fusion construct comprising two or more cojoined heterologous nucleic acid sequences, wherein the two or more cojoined heterologous nucleic acid sequences encode at least two enzymatic domains selected from the group consisting of a ketosynthase-acyltransferase, a chain length factor, an acyl carrier protein, and a cyclase.

67. The gene fusion construct of claim 66, wherein at least one of the two or more cojoined heterologous nucleic acid sequences is modified.

68. The gene fusion construct of claim 67, wherein at least one of the two or more cojoined heterologous nucleic acid sequences is shuffled.

A9 CONT.

69. A gene fusion construct comprising two or more cojoined heterologous nucleic acid sequences, wherein the two or more cojoined heterologous nucleic acid sequences encode at least two enzymatic domains selected from the group consisting of a phytoene synthase, phytoene desaturase, z-carotene desaturase, and beta-cyclase.

70. The gene fusion construct of claim 69, wherein at least one of the two or more cojoined heterologous nucleic acid sequences is modified.

71. The gene fusion construct of claim 70, wherein at least one of the two or more cojoined heterologous nucleic acid sequences is shuffled.

72. A hybrid protein comprising two or more heterologous enzymatic domains that participate in the same metabolic pathway, wherein at least one of the two or more heterologous enzymatic domains is encoded by a nucleic acid sequence that has been modified.

73. The hybrid protein of claim 72, wherein at least one of the two or more heterologous enzymatic domains is encoded by a nucleic acid sequence that has been shuffled.

74. The hybrid protein of claim 72, wherein two or more heterologous enzymatic domains are connected by one or more peptide linker sequences.

A10

76. The hybrid protein of claim 72, wherein the heterologous enzymatic domains that participate in the same metabolic pathway comprise one or more of phytoene synthase, phytoene desaturase, z-carotene desaturase, or beta-cyclase.

A10 cont.

77. The hybrid protein of claim 72, wherein the heterologous enzymatic domains that participate in the same metabolic pathway comprise one or more of diaminobutyric acid aminotransferase, diaminobutyric acid acetyltransferase, or ectoine synthase.

78. The hybrid protein of claim 72, wherein the heterologous enzymatic domains that participate in the same metabolic pathway comprise one or more of beta-ketothiolase, D-reductase, or poly(hydroxyalkanoate) synthase.

79. The hybrid protein of claim 72, wherein the heterologous enzymatic domains that participate in the same metabolic pathway comprise one or more of a ketosynthase-acyltransferase, a chain length factor, an acyl carrier protein, or a cyclase.

A11

81. The method of claim 80, wherein the at least two enzymatic domains comprise domains from plant enzymes selected from the group consisting of phytoene synthase, phytoene desaturase, z-carotene desaturase, and beta-cyclase.

82. The method of claim 80, wherein the at least two enzymatic domains are derived from proteins that participate in the same metabolic pathway.

A12

93. The method of claim 91, wherein at least about 80% of amino acid residues in the peptide linker are selected from the group consisting of alanine and glycine residues.

94. The method of claim 80, wherein the gene fusion construct further comprises one or more transcription regulatory sequences.

A13

96. The method of claim 80, further comprising introducing the gene fusion construct into a eukaryotic system.

A14

98. The method of claim 97, wherein the plant system is selected from the group consisting of Fragaria, Lotus, Medicago, Onobrychis, Trifolium, Trigonella, Vigna, Citrus, Linum, Geranium, Manihot, Daucus, Arabidopsis, Brassica, Raphanus, Sinapis, Atropa, Capsicum, Hyoscyamus, Lycopersicon, Nicotiana, Solanum, Petunia, Digitalis, Majorana, Cichorium, Helianthus, Lactuca, Bromus, Asparagus, Antirrhinum, Hererocallis, Nemesia, Pelargonium, Panicum, Pennisetum, Ranunculus, Senecio, Salpiglossis, Cucumis, Browaalia, Glycine, Lolium, Zea, Triticum, Sorghum, Malus, Apium, Narcissus, Docus, and Datura.

A15

100. A gene fusion construct comprising two or more cojoined heterologous nucleic acid sequences, wherein each nucleic acid sequence encodes one or more enzymatic

domains, and wherein at least one of the two or more cojoined heterologous nucleic acid sequences is derived from a plant.

101. The gene fusion construct of claim 100, wherein at least one of the two or more cojoined heterologous nucleic acid sequences is modified.

102. The gene fusion construct of claim 101, wherein at least one of the two or more cojoined heterologous nucleic acid sequences is shuffled.

103. The gene fusion construct of claim 100, wherein the two or more cojoined heterologous nucleic acid sequences encode at least two enzymatic domains selected from the group consisting of phytoene synthase, phytoene desaturase, z-carotene desaturase, and beta-cyclase.

A15 cont.

REMARKS

Applicants have amended claims 2-5, 7-12, 19, 23, 25-30, 38-43, 46, 50, 52-74, 76-79, 81-82, 93-94, 96, 98, and 100-103 and respectfully request entry of these claims prior to examination of the above-identified application. No new matter has been added to the application by way of the above amendments, which are entirely formal in nature.

CONCLUSION

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 510-337-7871.

QUINE INTELLECTUAL
PROPERTY LAW GROUP, P.C.
P.O. BOX 458
Alameda, CA 94501
(510) 337-7871
Fax (510) 337-7877

Respectfully submitted,

Angela P. Horne, Ph.D.

Angela P. Horne, Ph.D.
Reg. No. 41,079